

SEQUENCE LISTING

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<120> Method and Device for Optimizing a Nucleotide Sequence for the Purpose of Expression of a Protein

<130> B&B-135

<140> 10/539,208

<141> 2005-06-17

<150> PCT/EP03/14850

<151> 2003-12-23

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<151> 2002-12-23

<160> 32

<170> PatentIn version 3.3

<210> 1

<211> 435

<212> DNA

<213> Homo sapiens

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cagggcctgc ggggcagcct caccaagctc aagggcccct tgaccatgat ggccagccac 300
tacaagcagc actgccctcc aaccccggaa acttcctgtg caaccagat taccaccttt 360
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tacaagcagc actgccctcc tacccttgag acaagctgcg ccaccagat catcaccttc	360
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gcagggcctt ctaaaacaga agccaactgg gtgaatgtaa taagtgattt gaaaaaaatt	180
gaagatctta ttcaatctat gcatattgat gctactttat atacggaaag tgatgttcac	240
cccagttgca aagtaacagc aatgaagtgc tttctcttgg agttacaagt tatttcactt	300
gagtccggag atgcaagtat tcatgataca gtagaaaatc tgatcatcct agcaaacaac	360
agtttgtctt ctaatgggaa tgtaacagaa tctggatgca aagaatgtga ggaactggag	420
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gccggcctgc ctaagacaga ggccaactgg gtgaacgtga tcagcgacct gaagaagatc	180
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aacctcctgg atgacatgcc tgtcacattg aatgaagagg tagaagtcgt ctctaacgag	180
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tactgcccc caactccgga aacggactgt gaaacacaag ttaccaccta tgcggatttc	360
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aaatag	426

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aacctgctgg acgacatgcc cgtgaccctg aacgaggagg tggagggtgt gagcaacgag	180
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aagattccac gccaatcat cgttgactat tttgaaacca gcagcctttg ctcccagcca	180
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 <212> DNA
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<400> 8	
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ggcgtgatct tcctgaccaa gcggaacaga cagatctgcg ccgacagcaa ggagacatgg 240
gtgcaggagt acatcaccga cctggagctg aacgcctag 279

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<222> (42)..(42)
<223> n = a, t, g, or c

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<223> Hypothetical amino acid sequence.

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Glu Gln Phe Ile Ile Lys Asn Met Phe Ile Ile Lys Asn Ala
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<210> 11
<211> 9
<212> DNA
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<220>
<223> Combination DNA Sequence for amino acid SEQ ID NO: 10.

<400> 11
garcartty 9

<210> 12
<211> 9
<212> DNA
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<223> Combination DNA Sequence for amino acid SEQ ID NO: 10.

<400> 12
carttyath 9

<210> 13
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<400> 13
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<210> 14
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<400> 14
athathaar

9

<210> 15
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<210> 16
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<210> 17
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<210> 23
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 <313> (1)..(238)

<400> 23

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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Ser Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val
 210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
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11

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<210> 28
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